

A quantitative trait locus on chromosome 12 influences adipocyte number in baboons. AG COMUZZIE, LJ MARTIN, SA COLE, MC MAHANEY, J ROGERS, JE HIXSON, J BLANGERO. Southwest Foundation of Biomedical Research, San Antonio, TX 78227.

Increasing total body fat can greatly increase an individual's risk for development of a variety of chronic diseases (e.g., diabetes and coronary heart disease). Both adipocyte volume as well as number directly influences the total fat mass of an individual. Using a genome scan we have examined variation in adipocyte number in a sample of pedigreed baboons in an effort to identify possible genetic influences on this most fundamental of obesity-related phenotypes. This analysis used 202 animals distributed over 12 extended pedigrees. All of these animals were genotyped for 331 markers yielding an average map density of 7.2 centiMorgans. Linkage analysis was conducted using a variance component approach implemented in the program package SOLAR. Quantitative genetic analysis of adipocyte number detected an additive genetic heritability of 29%. The maximum LOD score detected in the multipoint linkage scan was 2.15 ( $p = 0.0008$ ) at *D12S84* on chromosome 12. No other chromosomal region showed any evidence of suggestive linkage. The 95% confidence interval for this quantitative trait locus (QTL) overlaps the region containing the insulin-like growth factor 1 gene (*IGF1*) which is a strong positional candidate gene for the regulation of cell growth and differentiation.

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Limb bone structure in flyers, gliders, and runners. J. RUNESTAD CONNOR, Department of Biological Sciences, Western Illinois University, Macomb, IL 61455

Bats use their limbs in very different ways than do other mammals. Correspondingly, this study considers whether bat humeral and femoral structural properties differ in predicted ways from those of primates, colugos, and scuirids.

Midshaft cortical area (CA), total subperiosteal area (TA), and moments of inertia (I) were calculated from radiograph measurements of wildshot museum specimens. Least squares regression was performed to compare slopes and elevations for bivariate comparisons between different groups. Findings will be further assessed via reduced major axis.

As expected, bat humeri are longer and

have greater CA than do the humeri of other mammals. However, the proportion of CA to TA is comparable to that in other mammals. Also, the proportion of humeral length to midshaft CA is only slightly higher than in primates such as cebid monkeys, and data sets overlap. Prevention of buckling may be more important than lightness in bat wings.

Bat femora are similar in the proportion of CA to length to the femora of generalized primates and nongliding tree squirrels. However, the proportion of bat femoral CA to TA is unusual -- their femoral cortices are quite thick. Bat hindlimbs are very active in roosting, flying, and climbing.

Comparisons of I values for anteroposterior and mediolateral planes do not separate bats from gliders or tree squirrels. Instead, generalized primates differ from the other groups. They have mediolaterally buttressed humeri and anteroposteriorly expanded femora, in comparison. Generalized primates are also surprising in that their humeri overlap in length with those of gliding squirrels and colugos.

Endocranial capacity of "Bodo Man" by 3D-CT. G. CONROY<sup>1</sup>, G. WEBER<sup>2</sup>, H. SEIDLER<sup>2</sup>, W. RECHEIS<sup>3</sup>, D. ZUR NEDDEN<sup>3</sup>, J. MARIAM<sup>4</sup>  
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The 600,000 year-old cranium from Bodo, Ethiopia, is the oldest and most complete early Middle Pleistocene hominid skull from Africa. Using three-dimensional computed tomography (3D-CT) techniques, its endocranial capacity (taken as a surrogate of brain volume in paleoanthropological studies) is determined to be ~1300 cc. From this determination, several important implications emerge concerning current interpretations of 'tempo and mode' in early hominid brain evolution: (i) already by the early Middle Pleistocene, at least one African hominid species, *Homo heidelbergensis*, had reached an endocranial capacity within the normal range of modern humans; (ii) in spite of its large endocranial capacity, Bodo's Encephalization Quotient (EQ) of ~3.8 falls below that found in a large sample of *Homo sapiens* (both fossil and recent) and Neandertals; (iii) the greatest burst of brain expansion in the

*Homo* lineage may not have been in the last several hundred thousand years, but rather much earlier in the Lower to early Middle Pleistocene.

How many species at Paşalar? A study in molar morphology. L.A. COOK and L.C. AIELLO, Department of Anthropology, University College London, England WC1E 6BT, P.J. ANDREWS, Natural History Museum, London England SW7 5BD

The Miocene site at Paşalar, Turkey has been under anthropological scrutiny for thirty years. One of the larger questions that have undergone considerable study has been whether or not a second species, apart from *Griphopithecus alpani*, exists within the collection of fossils from that site. This paper looks at that question from the point of view of the morphology of the molar teeth. Nine morphological characteristics were identified and combined with the metrical data from previous studies. Eight hundred forty-two molars from the site were divided into six categories including the first, second and third lower molars along with the three corresponding upper molars. The unworn molars were analysed with an extant group of the three sub-species of chimpanzees. In addition, an analysis was done using *Griphopithecus* alone. Since the analysis of combined metrical and non-metrical data is uncommon, the use of a variation on components analysis called combined co-ordinates utilising Gower's Similarity Coefficient was undertaken. The results of this method demonstrated a separation of a small (13.5-15.9%) group that differs in morphology from the remainder of the sample. This compares to 8 to 10% found in previous studies. Both the combined *Griphopithecus* / *Pan* group and *Griphopithecus* sample alone showed the same results. The distinguishing characteristics of the lower molars that formed the second group were the presence of a buccal cingulum, 7<sup>th</sup> cusp and a metaconid fissure. These were lacking in the second group. The upper molars maintained the presence of a mesial marginal ridge and a 5<sup>th</sup> cusp while a centre cusp appeared to separate out the second group. Those separations were accepted as evidence of a second species.

The Upper Paleolithic-Mesolithic Dental Complex in Europe: A. COPPA, A. CUCINA, R. VARGIU, Università di Roma "La Sapienza", Italy; D. MANCINELLI, Università de L'Aquila; M. LUCCI, Università di Cagliari, Italy.

Recent research still in progress on dental morphological traits (ASU System) clearly distinguishes the Italian Upper Paleolithic-Mesolithic populations from later ones. This is due to a different dental morphology, which can be considered characteristic of this group. Based upon the

analysis of the single-trait frequencies on 108 individuals, it was possible to identify what was called an "Italian Upper Paleolithic-Mesolithic dental complex", characterized by trait frequencies which are either much higher or lower than in the more recent samples. The analysis spread to European samples in order to detect if such pattern could be shared also by the populations beyond the Alps. Coeval samples from France (91 individuals), Czech Republic, Croatia and Slovakia (for a total of 67 individuals) have been scored for 79 morphological traits, and 26 of them have been used in this study (16 maxillary and 10 mandibular). Despite some minor differences, the European samples show a strong similarity with their Italian coevals, particularly as the high-frequency traits are concerned. The Upper Paleolithic samples have then been compared with more ancient samples, that is Krapina (40 individuals), the European Neanderthals (89 individuals), the Asiatic Neanderthals (16 individuals), the Levantine anatomically modern humans (Qafzeh and Skull, 26 individuals) as well as with the more recent Palestinian Natufians (222 individuals). Principal Component Analysis and a Maximum Likelihood method (the latter tested by bootstrapping) have been applied to the percent frequency of the traits. A chronological separation between Upper and Middle Paleolithic arose from both analyses, further confirming the similarities between the Italian dental complex and the European one. As Dolni Vestonice is the more ancient and eastern among our Upper Paleolithic samples so far analyzed, a very preliminary analysis was run to test what the distances with even more ancient groups could have been. A pair-wise test placed Dolni Vestonice with Krapina and with the Levantine anatomically modern humans (Qafzeh and Skull). These preliminary results do not rule out the possibility that the above sample from the Czech Republic might have its line of ancestry with both Krapina and the anatomically modern humans from the Levantines. Supported by the "Progetto Finalizzato CNR, Beni Culturali" 96.01106.PF36 and 97.00623.PF36, MURST 40%/97.

Aging rhesus macaques: male and female social behaviors. J. CORR and D.E. CREWS, The Ohio State University, Columbus, OH 43210

Available data on social aging in nonhuman primates are conflicting and limited to females. We obtained 624 hours of observational data on Cayo Santiago during 1997-8 to investigate the relationship between chronological age and social behavior in male and female (N=42) rhesus macaques (*Macaca mulatta*.) These data are used to examine age and sex-based individual and group social behaviors by age cohort.

Female (N=24) social behavior received ( $r = -.38$ ,  $p = .04$ ) and directed ( $r = -.42$ ,  $p = .04$ ) are both negatively correlated with age. In males (N=18), age and social behavior, both received ( $r = .55$ ,  $p = .04$ ) and directed ( $r = .50$ ,  $p = .04$ ), are positively correlated. Females show a negative correlation between age and network size ( $r = -.64$ ,  $p = .0007$ ), and age and time in social contact ( $r = -.43$ ,  $p = .04$ .) Males show a low, positive correlation between age and network size ( $r = .35$ ,  $p = .155$ .) but a substantial correlation between

age and time in social contact ( $r=.50$ ,  $p=.034$ .) This suggests that while females are increasingly less social with advancing age, males may be increasingly more social.

In addition, qualitative changes may occur in social networks over the lifespan. Females of all ages spend the majority of their total social contact time with daughters. Young and middle-aged males spend the majority of their time with adult females. "Aged" males spend 80% of their social time with infants and yearlings. These results illustrate age and sex-based differences in male and female social behaviors. These social behaviors also vary by dominance rank and relatedness of partners.

Biological aging and survivorship among Mennonites of the Midwest. M.H. CRAWFORD, University of Kansas, M. UTTLEY, Lander University, and R. DUGGIRALA, University of Texas Health Science Center, San Antonio.

From 1979 to 1982, a research program on Mennonite communities of Kansas and Nebraska yielded a wealth of information about the processes of biological aging. This study was based on a total of 1200 participants, whose aging was assessed by sensory data, neuromuscular function, blood chemistry, anthropometric measurements and other health-related information. In addition, several followups on survivorship were conducted in the 1990s. The data collected from these communities are unique because: (1) rural, farming communities are represented; (2) populations are relatively homogeneous culturally and genetically; (3) the samples included equal numbers of males and females; (4) the inter-disciplinary nature of this study permitted a bio-cultural analysis of the causes of biological aging.

Variance decomposition methods were employed to test models of the genetic contribution to the complex phenotype, biological aging. This phenotype was defined as the standardized residuals of a regression analysis between chronological age and neuromuscular performance.

Based on discriminant function analysis, the best predictors of death from the 1979-1982 sample were: age, blood urea nitrogen, BUN/creatinine, low density lipoproteins (LDL) (only in women), glucose levels in men. Most of the variables which separate the surviving from the deceased Mennonites are associated with declining renal functions. Asymptomatic and incipient disease conditions were identified that affect differential survivorship. Supported in part by a grant from NIH AG01646-03.

Predictive modeling of stabilization of balanced polymorphisms. T.C. CRAWFORD and S.M. FORD, Southern Illinois University, Carbondale, IL 62901-4502.

A balanced polymorphism arises in a population when multiple alleles at a particular genetic locus are maintained at stable frequencies. The most frequent cause of these stable polymorphisms appears to be the balancing of selective forces due to heterozygote advantage (heterosis or overdominance). The prevalence of sickle cell anemia in African populations, where malaria is a powerful selective agent, is a widely recognized example of this situation. Several other balanced polymorphisms are argued to be the result of heterosis, including other anti-malarial hemoglobin variants (such as HbC and thalassemia) as well as cystic fibrosis (CF) in people of European ancestry and Tay-Sachs disease in Ashkenazic Jews of Eastern European ancestry.

Investigating the rates at which allele frequencies for these lethal genetic disorders increase to stabilization when heterozygotes have a selective advantage are of great import. The vast majority of available data on individual human populations for heterotic conditions are single point-in-time studies. Time successive data are almost entirely non-existent, certainly none with a time depth to indicate rates of change to attainment of stabilization. Traditional population genetics provides theoretical mathematical formulae to estimate rates of stabilization, but these models are deterministic, are based on estimates of relative fitness, and provide only a single estimated rate value. A modeling program, *Evolve* (The BioQUEST Library, Academic Software Development Group), allows an expanded consideration of likely times to stabilization, including manipulation of a variety of factors (including survival rate, reproductive rate, population size, and "carrying capacity") and an element of chance or randomness, to simulate various real-world situations.

This program was used to investigate possible times-to-stabilization of theoretical populations modeled on several real human examples. These include West and East African populations in apparent balanced polymorphic states for the sickle cell trait but at different equilibrium points and with different demographic profiles. Estimated rates to and degree of stabilization are compared to published data and to estimates based on mathematical formulae.

The variability present in West African populations appears explainable in terms of demographic features. Time-to-stabilization often appears longer than estimates from mathematical formulae. Several errors in computation in the early literature, frequently repeated, are corrected.

Diagonal gait in Primates: its role in stability on arboreal substrates. R.H. CROMPTON, Y. LI, W.WANG, R.SAVAGE, R.C. PAYNE and M.M. GUNTHER, Human Anatomy and Cell Biology, University of Liverpool, PO Box 147. Liverpool L69 3GE UK.

Primates are exceptional among mammals in their habitual use of diagonal rather than lateral gaits. This fact has in the past been attributed to factors as diverse as hindlimb dominance and the problems of quadrupedalism on compliant substrates. Using simultaneous two-camera videography and Kistler forceplate measurements, we investigated the mechanics of quadrupedalism in a variety of primates and non-primates including domestic dogs,

coatis, ruffed lemurs, capuchins, Sulawesi macaques and common chimpanzees. With the exception of chimpanzees and dogs, we compared motion on compliant and non-compliant substrates using a forceplate superstructure, and for the ruffed lemur and coati, carried out direct measurement of turning forces using a digital torque gauge. Contrary to the common perception, our kinematic data show that lateral gaits are in fact commonly adopted by ruffed lemurs, while some dogs prefer diagonal gaits. Substrate compliance, per se, does not exert a significant effect on vertical or sagittal forces in either our primate sample or the coati. However, data on lateral forces and torques show that the grasping extremities and diagonal gaits of higher primates allow them to apply balanced torques to narrow supports, while mammals using lateral gaits appear to rely on tail movements to balance the body.

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**Historical biogeography of the tamarins and squirrel monkeys: Evidence from molecular phylogeny, estimates of divergence times, and geological events.** S. CROPP, Department of Ecology and Evolution, University of Chicago, Chicago, IL 60637, and S. BOINSKI, Department of Anthropology and Division of Comparative Medicine, University of Florida, Gainesville, FL 32611.

There are many hypotheses concerning the historical dispersal of New World monkeys across South America. Most are based on the current distributions of extant species and their similarities to one another. A recent study by Cropp et al., (1999) tested two phylogenetic hypotheses concerning the dispersal of tamarins (genus *Saguinus*) across South America. One phylogenetic hypothesis was premised on ecological factors relating to body size, and the other on the theory of metachromism. Using a molecular phylogenetic analysis, Cropp et al., (1999) rejected both of these hypotheses and hypothesized that tamarins probably dispersed in two major waves from an origin somewhere south of the Amazon and west of the Rio Madeira and that this dispersal was most likely a pre-Pleistocene occurrence.

In an effort to further test this new biogeographic hypothesis, we set out in the present study to demonstrate that the same dispersal pattern also holds true for another group of New World primates with approximately the same geographic distribution as tamarins. Squirrel monkeys (genus *Saimiri*) are larger in body size than tamarins, but are subject to similar physiogeographic barriers to dispersal. Recent behavioral and genetic studies of squirrel monkeys (Boinski & Cropp, 1999; Cropp & Boinski, 1999) have clarified the phylogenetic relationships among *Saimiri* species. These data reveal that squirrel monkeys have a similar geographic pattern of phylogenetic relationships as tamarins, supporting the biogeographic hypothesis set forth for tamarins. We have also estimated divergence times between species in these two genera based on fossil evidence and the molecular data. Thus, we are able to examine speciation for both

genera superimposed on a background of known geological events. This work has been supported by NSF grants DEB - 9411169 and DBI - 9750030 to SC and SBR - 9722840 to SB and other grants to SB.

**Within-group human variation in the Asian Pleistocene: an assessment of the three Upper Cave crania.** DL CUNNINGHAM, University of Missouri, Columbia, MO 65211 and DJ WESCOTT, University of Tennessee, Knoxville, TN 37996.

The first occurrence of the modern composition of human populations has been a subject of debate. Some contend that modern within-group distribution of craniometric traits is a relatively recent phenomenon, while others claim it is much more ancient. The three anatomically modern Upper Cave crania from Zhoukoudian, China, provide one of the best samples available for addressing this question because they are spatially and temporally restricted. Research on the 25,000 year old Upper Cave fossils usually only includes UC 101 and UC 103 because of postmortem damage to UC 102's cranial vault. Although the vault of UC 102 is unsuitable for metric analysis, the face is undamaged, allowing for most facial measurements to be accurately performed. Therefore, in this study we use facial dimensions to compare the three Upper Cave specimens, and we evaluate whether the variation seen among them is larger than that observed in extant populations.

The three Upper Cave crania are compared to a worldwide sample of modern ethnic groups drawn from a data collection at the University of Tennessee that combines Howells' data with data from additional modern Amerindian groups. In the analyses, UC 102 is treated alternately as a male and as a female, since there is disagreement over this specimen's sex. Multivariate results show that the Upper Cave specimens exhibit significantly more variation than do individuals within more recent human populations, especially if UC 102 is considered female.

The implications are twofold: either the Upper Cave sample does not represent a breeding population, especially not a family unit as has been postulated, or, if these three individuals are from the same breeding population, they exhibit more variation in their facial dimensions than do extant populations. This second implication suggests that the within-group distribution seen in modern ethnic groups could indeed be a relatively recent phenomenon.

**Craniodental variation in *Galagoides* and *Microcebus* and its implications for the paleotaxonomy of small-bodied Eocene primates.** F.P. CUOZZO, Anthropology, University of Colorado, Boulder, CO 80309-0233

The small-bodied nocturnal prosimians *Galagoides* and *Microcebus* have undergone a great deal of taxonomic



revision in recent years (e.g. Bearder et al., 1995; Atsalis et al., 1996; Honess, 1996; Wickings et al., 1998; Zimmerman et al., 1998). Because dwarf galagos and mouse lemurs are among the modern analogs for small-bodied Eocene primates (Covert, 1995), their taxonomic revision has implications for understanding the paleotaxonomy of these extinct forms. Therefore, knowledge of the patterns of variation exhibited by these extant groups is an integral part of delineating the paleotaxonomy of small-bodied Eocene primates. Here I present data on the patterns of craniodental variation seen in *Galagoides* and *Microcebus*.

Craniodental measurements were taken and a series of morphological observations were made on museum specimens of *Galagoides demidoff* and *Microcebus murinus*. Results indicate that substantial morphological variation exists in both geographically restricted and more dispersed samples. For example, in several of the *Microcebus* specimens, which were all collected at the same locality, the morphology of  $M^1$  varies in that a distinct cusp distolingual to the hypocone is present. This cusp distorts the overall size and shape of  $M^1$  so that in a fossil assemblage, an isolated  $M^1$  might easily be viewed as representing a distinct taxon. Traits showing varied polarity in the less geographically restricted *Galagoides* sample include  $M^{1-2}$  conules,  $P^3$  hypocones, and  $P^{2-3}$  protocones. In contrast to this morphological pattern, there is a greater amount of metric variation in the geographically less restricted *Galagoides* sample than in the *Microcebus* sample. For example, the degree of variation in  $M^1$  is greater for *Galagoides* ( $n = 67$ ,  $CV = 6.56$ ) than for *Microcebus* ( $n = 55$ ,  $CV = 3.87$ ). These results suggest that caution must be used in interpreting taxonomic diversity in fossil assemblages based on either metric variation in geographically dispersed samples or morphological traits that exhibit varied polarity within extant taxa.

The ecological diversity of the fossil primate community from La Venta, Colombia. C. E. CURRIE, Department of Anthropology, Arizona State University, Tempe, AZ 85287

The middle Miocene deposits of La Venta, Colombia, have produced a striking variety of fossil platyrrhine species. With as many as nine different genera, the taxonomic diversity of this fossil group rivals that of some extant platyrrhine communities. It is also important, however, to consider diversity in ways other than species richness. This study compares the fossil community with modern day counterparts from an ecological point of view, to provide greater insight into the diversification and paleoecology of Miocene platyrrhines.

To avoid the problems of time-averaging, only the five species of fossil platyrrhines thought to be synchronic and sympatric were considered in this analysis. 12 extant primate communities were chosen from a variety of habitats in the neotropics. Values for two important ecological variables, body size and molar shearing quotient, were available for all fossil and extant species.

These values were log-transformed and plotted against each other to create a two-dimensional ecospace for each community. The resulting polygons were then used to compare the overall ecological diversity of the fossil and extant groups.

The results indicate that the fossil community shares the most ecospace with extant groups in mosaic habitats and terra firme forests, and little with those in extremely wet or extremely dry environments. The overall shape of the polygon formed by the fossil species bears the greatest resemblance to extant communities found in mosaic habitats such as Raleighvallen, Surinam. This is consistent with Kay and Madden's (1997) reconstruction of the Miocene site as a "heterogeneous riparian mosaic". Compared with such sites, however, the ecospace of the fossil community is somewhat restricted and tends to occupy the central portion of the space defined by these extant communities. This suggests that ecological diversity of platyrrhines was more limited in the Miocene than in the present day.

Genotype by smoking interaction: Evidence for effects on lipids and lipoproteins in Mexican Americans. S.A. CZERWINSKI, M.C. MAHANEY, D.L. RAINWATER, J.L. VANDEBERG, J.W. MACCLUER, J. BLANGERO. Department of Genetics, Southwest Foundation for Biomedical Research, San Antonio, TX 78245.

Several studies have noted the positive association between cigarette smoking and atherogenesis. Many association studies of candidate genes have reported a differential genetic effect between smokers and non-smokers. This study seeks to determine whether a significant gene by smoking interaction exists on lipid and lipoprotein risk factors for atherosclerosis, including plasma triglyceride (TG) levels, HDL cholesterol (HDL-C) and median LDL particle diameter (LDL-MPD). The sample consisted of 1392 Mexican Americans distributed in 42 pedigrees, ranging in age from 16 yrs to 92 yrs. Participants were classified as either current smokers ( $n=320$ ) or non-smokers ( $n=1063$ ). Fasting plasma TG and HDL-C were assayed using standard clinical chemistry protocols. To assess LDL-MPD plasma LDLs were resolved with gradient gel electrophoresis and cholesterol was stained with sudan black B. Separate quantitative genetic analyses were carried out for TG, HDL-C and LDL-MPD using a maximum likelihood-based variance decomposition approach simultaneously adjusting for age and sex. Initial heritability estimates demonstrated all three traits to be significantly ( $p<0.001$ ) heritable ( $h^2$  from 0.50-0.54). To test for a gene by smoking interaction, additional smoking status-specific variance terms were included in the model, as well as a genetic correlation term between smokers and non-smokers. Comparisons of nested models revealed strong evidence ( $p<0.01$ ) of a gene by smoking interaction effect on all three traits. These results indicate that the gene or suite of genes regulating each of these phenotypes is likely the same in smokers and non-smokers, but that smoking may alter the expression of genes, particularly those influencing TG, and LDL-MPD.

Gnathic morphology and feeding ecology in papionin primates. D.J. DAEGLING, Department of Basic Medical Sciences, California College of Podiatric Medicine, San Francisco, CA 94115, and W.S. MCGRAW, Department of Anthropology, The Ohio State University, Mansfield, OH, 44906.

A consensus has recently emerged, based on molecular as well as morphological evidence, that the mangabeys do not constitute a natural group by cladistic criteria. The genus *Cercocebus* may now be regarded as the sister taxon of *Mandrillus* while *Lophocebus* is phyletically allied with *Papio*.

Certain aspects of feeding behavior mirror these proposed relationships. *Cercocebus* and *Mandrillus* display features in the postcanine dentition (molarized P4s, heavy attrition) consistent with field observations that these animals habitually masticate hard objects. In contrast, *Lophocebus* and *Papio* differ from these taxa by their possession of enlarged incisors, which is presumably related to an emphasis on incisal preparation of food items. In fact, *Lophocebus* differs from *Cercocebus* in feeding ecology by its more frequent incisal preparation of hard objects.

Between the mangabeys, the emphasis on mastication versus incision of tough food items has specific biomechanical implications. It is predicted that incision is associated with relatively large parasagittal bending moments while mastication will be characterized by enhanced transverse bending moments. To test the hypothesis that contrasting feeding behaviors are reflected by differences in mandibular morphology, we measured functionally relevant variables on a sample of *Cercocebus* and *Lophocebus*. The same variables were also measured on samples of *Papio* and *Mandrillus* to assess whether differences between mangabeys are paralleled by their respective sister taxa.

Mandibular form differs significantly between *Lophocebus* and *Cercocebus*, and these differences are functionally consistent with their disparate feeding behaviors. Differences between *Papio* and *Mandrillus* were also found, but these do not necessarily conform to the pattern discriminating the two mangabeys.

Health on the periphery of the Aztec empire: The human remains from Xaltocan, Mexico, D.F. M.E. DANFORTH, Department of Anthropology and Sociology, University of Southern Mississippi, Hattiesburg, MS 39406-5074.

Although the Aztecs developed one of the most well-known states in the New World, relatively little work has been done at its more marginal regions. These areas are crucial for study, however, since the success of the empire generally hinged on their integration into the larger political and economic structure. One site located on the peripheries of power is Xaltocan, which was situated on a lake in the northern part of the Valley of Mexico. Originally it was the home of the Otomis, but

its inhabitants were reportedly forced out in A.D. 1430 and replaced by Aztecs.

Recent archaeological work at Xaltocan has uncovered the well-preserved remains of some ten individuals, dating to both the early and late Postclassic. Seven skeletons belong to young children aged birth to five years, and the other three to young adult males. The general health reflected in the series appears to be good across all time periods according to most indicators. In the juveniles, no enamel hypoplasias were seen in the deciduous teeth, and caries were few. Single instances of porotic hyperostosis and osteomyelitis were present, and neither were particularly severe. Hypoplasias were also rare among the adults as were caries, but relatively heavy calculus deposits were noted. No other pathologies were observed.

These preliminary findings may be compared with those from most precontact Mesoamerican centers in which the health of inhabitants, especially that of young children, was highly compromised. Thus, the lower population density of Xaltocan appears to have eased the pathogen load. Furthermore, the results also suggest the residents of the site were not at a disadvantage in terms of access to nutritional resources, either before or after incorporation into the empire, despite their more peripheral location. These findings will be discussed in light of future research, including isotope analysis.

Do different kinds of cranial deformation affect the incidence of wormian bones in human crania? V.DEAN O'LOUGHLIN, Medical Sciences Program, Indiana University, Bloomington, IN 47405.

In 1897, Dorsey was among the first to suggest that pressure on the skull (from cultural cranial deformation) may influence the incidence of wormian bones. Since then, many researchers have examined this hypothesis. Results varied, and several hypotheses have been presented concerning the etiology of wormian bones: 1) they are under genetic influence, 2) environmental stressors (such as cranial deformation) primarily affect their incidence, or 3) the presence of wormian bones is genetically determined, but the number of bones may be influenced by external factors. Previous studies examined skulls exhibiting a few kinds of cranial deformation only. Many different cranially deformed groups should be analyzed together to explore this possible interrelationship.

This research examines the effects of many kinds of cranial deformation on the incidence of wormian bones. A sample of 127 skulls were examined, and came from many different New World archaeological sites. An undeformed cranial sample was compared to the following cranially deformed groups: 1) occipital, 2) lambdoid, 3) annular, 4) fronto-vertico-occipital, 5) parallelo-fronto-occipital, 6) sagittal synostosis. Degree of cultural cranial deformation was recorded. Number of wormian bones along all calvarial sutures was calculated for each skull. Group means were analyzed using Kruskal-Wallis Oneway ANOVA statistical tests.

Results indicate that all kinds of cranial deformation affect the frequency of *some* kinds of wormian bones. In particular, all cranially deformed groups exhibited significantly greater frequencies of ossicles in the lambdoid suture. Apical, parieto-mastoid, and occipito-mastoid wormian bones also appear with greater frequency in culturally deformed skulls. Further, different degrees of cultural deformation all had more lambdoid wormian bones than the undeformed group. These results suggest that wormian bone development in the posteriorly-placed sutures may be affected more by environmental stressors than their anteriorly-placed counterparts.

An experimental study of deception in ringtailed lemurs.  
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Because of their socioecological similarities, ringtailed lemurs and cercopithecines have long been compared. One difference is that cercopithecines have been observed to spontaneously deceive their groupmates but ringtailed lemurs have not. This difference may be due to observational bias, differential opportunities for deception, or a difference in social cognition.

In order to distinguish among these possibilities, I presented opportunities for ringtailed lemurs to deceive each other in the 'Menzel' paradigm. Here a subordinate animal is informed of a favored food's location and then the informed individual and an uninformed dominant animal are simultaneously released into an enclosure. Previous work has shown that an informed mangabey can learn to consistently lead an uninformed dominant away from the food (i.e. deception), thereby increasing its own food intake.

Two male and two female ringtailed lemurs were initially trained to use a visual signal to find food at one of eight feeding sites in an outdoor enclosure. During experimental trials, an informed male was simultaneously released with an uninformed dominant female. The following results were obtained. First, females spontaneously followed males to baited food sites and usually monopolized the food. Second, after consistently moving directly to the food and losing it to the female, males employed alternative tactics. Third, some alternatives were effective (e.g. moving initially away from food and then towards it) but others were not (e.g. not moving towards any food site). Finally, unlike mangabeys, male ringtailed lemurs did not consistently employ effective alternative tactics. These results are consistent with the hypothesis of a cross-species difference in social cognition.

New methods for evaluating the potential impact of character dependencies on hominid cladograms.  
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The phylogenies produced by cladistic analysis are primarily a result of the characters used. Ideally, all characters used in a cladistic analysis are independent. To avoid bias, the state of one character should not be functionally related to the state of any other character in the analysis. Determining whether characters are independent requires elucidation of the genetic, developmental, and functional basis of the characters. Such information, while it will ultimately clarify such issues is not currently available for most characters used in hominid systematics.

So while the presence of dependent characters in a cladistic analysis can influence the results, we currently lack the ability to determine which characters might be dependent on each other. It would therefore be useful to have a means of estimating the potential impact of character linkages on a given cladogram. Three methods to do so are presented here.

Character Importance Ranking identifies the characters that are most influential in shaping a cladogram, as these should be priority targets for developmental and functional investigations. The Resistance to Character Linkage index provides a measure of the relative sensitivity of cladograms to potential linkages between characters. Linkage Distance Between Cladograms identifies the characters linkages required to transform one cladogram into another. These methods can be used to assess the potential impact of character dependencies in published cladograms of hominid relationships.

The Behavior of extinction: Predicting the incidence of lemur populations in fragmented habitats of SE Madagascar. DEHGAN, A. and B. PATTERSON, Committee on Evolutionary Biology, The University of Chicago, IL 60637 and Division of Mammals, Field Museum of Natural History, Chicago, IL 60605, and P.C. Wright, Department of Anthropology, SUNY-Stony Brook, Stony Brook, NY 11794.

We do not understand why some animals persist while others go extinct. Although the Theory of Island Biogeography, and the other biogeographic theories that subsequently built on it, have allowed researchers to predict the number of species that an island – such as a newly-created habitat fragment – can support, these

theories have failed to explain the proximate mechanisms driving local extinctions in the fragments, the relative importance of those mechanisms, or why fragmentation and its associated effects impact closely related organisms differently.

A synthesis of biogeographic theory and behavior provides a conceptual framework to explain the effects of habitat fragmentation by tying the landscape-level patterns of fragmentation-driven extinction and local behavioral and ecological processes. When habitat fragmentation alters the environment through simplification and alteration of the ecosystem, behavior becomes the leading edge of adaptation to such changes. In our study, we examine the role that behavior, in particular social structure and foraging, and phylogenetic constraint on such behavior (behavioral plasticity), play in determining the ability of lemurs to survive forest fragmentation in Madagascar.

This poster presents a theoretical model that predicts the impact of different behavioral and demographic characteristics, and the degree of plasticity as constrained by a species evolution, on the incidence and expected persistence of twelve lemur species in S.E. Madagascar, and the preliminary results from testing the model's efficacy in the field.

Origins of the Polynesian people: new insights from the Y chromosome. R. DEKA, Department of Environmental Health, University of Cincinnati; B. SU, L. JIN, R. CHAKRABORTY, Human Genetics Center, University of Texas at Houston; J. MARTINSON, Department of Biological Anthropology, Oxford University; P. UNDERHILL, P. OEFNER, Department of Genetics, Stanford University; S.T. MCGARVEY, Department of Medicine, Brown University; N. SAHA, Department of Genetics, Australian National University; M.D. SHRIVER, Department of Anthropology, Pennsylvania State University; J. CHU, Institute of Medical Biology, Chinese Academy of Medical Sciences, Kunming, China.

Polynesian origin has remained a controversial issue. Two competing hypotheses, one postulating Taiwan as the putative homeland - the "express train model", and the other asserting a Melanesian origin - the "entangled bank model", have received considerable attention. The former, based on linguistic and archeological evidence, has received support from recent mitochondrial data. We have studied 19 biallelic polymorphisms on the Y chromosome in a sample of 551 male individuals from 36 populations living in Southeast Asia, Taiwan, Micronesia, Melanesia and Polynesia and identified a total of 15 haplotypes. Surprisingly, nearly none of the Taiwanese haplotypes were found in Micronesia and Polynesia. Likewise, a Melanesian-specific haplotype was not found among the Polynesians. However, all of the Taiwanese, Polynesian and Micronesian haplotypes were found in the extant Southeast Asian populations. Evidently, the Y chromosome data do not lend support to either of the prevailing hypotheses. Further, genetic divergence between

the Taiwanese and the Micronesian/Polynesian populations is twice as large as that between the Southeast Asians and either of these island populations. The most plausible explanation of our data is that both the Taiwanese and the Polynesian populations derive their ancestry in Southeast Asia. However, colonization of Polynesia had occurred via a route independent of the expansion toward Taiwan.

Supported by grants from the National Science Foundation and the National Institutes of Health, USA, and the Chinese National Natural Science Foundation.

Reversal of asymmetric growth in the cranial base following neurocranial surgery in unicoronal craniosynostosis. V.B. DeLEON, T.M. COLE, III, S. LELE, J.L. MARSH, J.T. RICHTSMEIER, Johns Hopkins University School of Medicine, Baltimore, University of Missouri, Kansas City, University of Alberta, Edmonton, and Washington University School of Medicine, St. Louis.

Unicoronal craniosynostosis (UCS) is associated with directional asymmetry of the entire craniofacial complex. Due to the interrelated nature of growth in the neurocranium and cranial base, unilateral fusion of the coronal suture alters growth trajectories in the cranial base and produces an asymmetric basicranial morphology. Treatment involves surgical release of the suture and reconstruction of the neurocranium, resulting in a more symmetric vault. The purpose of this study is to determine whether release of the coronal suture and reshaping of the neurocranium affects the degree of asymmetry seen in the cranial base.

Our patient sample consisted of preoperative and postoperative children diagnosed with UCS. We created three-dimensional computer reconstructions of crania from patient CT scan data and from these collected coordinate data for 22 landmarks on and around the cranial base. Euclidean Distance Matrix Analysis (EDMA) was used to compare the degree of asymmetry between the fused and unfused sides of the cranial base within samples of preoperative and postoperative patients.

The results of this study demonstrate that the cranial base in postoperative UCS patients is more symmetric than in preoperative patients with a fused coronal suture. Following release of the neurocranial restraint, linear distances with previously limited growth show increased growth at a rate sufficient to compensate for and reverse the previously existing asymmetry. These results indicate that forces impacting the neurocranium have an associated impact on growth patterns in the cranial base, supporting the concept of interrelated growth in functional components of the cranium. This study suggests that some level of symmetry is inherent to the cranial complex and has further implications for research involving asymmetry in the brain and developing craniofacial complex.

This work was supported by an NIDCR grant to JTR.



New hypothesis on hominoid bipedalism. Y. DELOISON, CNRS, Dynamique de l'évolution humaine, Paris, France.

This paper presents the results of a study of approximately 100 fossil foot bones of australopithecines from Ethiopia, Tanzania and South Africa, between 1 and 3 millions years old. It is also based upon analyses of ten fossil footprints from Laetoli (Tanzania) (casts made by Ron Clarke at the time of the discovery in 1978), and the hind limbs of StW 573 from Sterkfontein discovered by Ron Clarke in 1998. This provided essential information about hominid locomotion.

The anatomical features of the hind limbs of australopithecines indicate the possibility of two modes of locomotion: arboreal and bipedal in the same organism. The arboreal and bipedal characters are found together on the same bones.

On the bones from Hadar (Ethiopia), I observed typical arboreal features but also characters specific to australopithecines. On the bones from South Africa, I found three groups of bones : 1) those with arboreal characters; 2) those with bipedal characters, and 3) other bones that have arboreal characters associated with bipedal characters in relation to the observed face of the bone.

All these anatomical and biometrical studies induced me to better understand the locomotion of the australopithecines and to elaborate a new hypothesis of the origin of man.

Thus, Lucy has bipedal characteristics, but she also has divergent big toes like those used by the apes of today to climb trees. Evolution never goes backward. Thus the human foot, highly specialized for bipedal use, cannot have been derived from a foot adapted to climbing trees, which is also highly specialized but in a different way.

A group of Primates would have existed about 15 millions years ago, practicing a particular form of bipedalism. They would have been the ancestor of *Pongo*, *Gorilla*, *Pan*, australopithecines and *Homo*. Then the apes became more arboreal and quadrupedal. Note that apes practice knuckle-walking but monkeys do not. The australopithecines, as apes, practice two forms of locomotion, while our ancestor became permanently bipedal.

Cortical bone distribution in the femoral neck of strepsirrhine primates. B. DEMES, W.L. JUNGERS, Anatomical Sciences, SUNY at Stony Brook, NY 11794, and C.J. WALKER, 1200 Cherokee Drive, Waycross, GA 31501.

The distribution of cortical bone in the femoral neck has figured prominently in attempts to reconstruct locomotion of fossils. Humans and the Hadar hominids have low ratios of superior over inferior cortical thickness, whereas African apes and atelines have higher ratios and, hence, a more even distribution of cortical bone in the femoral neck. In this study, we present and analyze data on cortical thickness in the femoral neck of a diverse sample of 186 strepsirrhine primates representing 26 species.

Measurements were taken on anteroposterior x-rays of

femora. In addition to cortical thickness, length and depth of the femoral neck were determined, as well as its angle with the shaft. Second moments of area were calculated assuming that the neck is a hollow cylinder with variable wall thickness. In all species the inferior cortex is clearly thicker than the superior cortex. Thickness ratios do not differentiate between locomotor groups. The loridid climbers are not characterized by a more even bone distribution. Thickness ratios do not correlate with neck length, neck-shaft angle or body mass, which would be expected if the neck behaved like a cantilever beam in bending. Second moments of area scale with the product of body mass times neck length (a proxy of the bending moment experienced by the neck) with slight positive allometry. This relationship is driven overwhelmingly by size, with neck length being a minor contributor. Exceptions exist, but galagid leapers tend to have stronger femoral necks for their body size, and loridid climbers weaker necks.

The results indicate that the strepsirrhine femoral neck is probably not acting like a cantilever beam with bending as a predominant loading regime. Strepsirrhines have short femoral necks and stress distribution may not be similar to that expected based on simple beam theory. The inferior cortex may need reinforcement because of its sharper curvature. As the femoral neck is not a hollow tube, trabecular bone (ignored in this study) may contribute importantly to its mechanical strength. The ratio of superior to inferior cortical thickness is not a good predictor of locomotor mode, at least in strepsirrhine primates.

Human brain growth is not unique. A comparative study of eutherian and marsupial carnivores/omnivores and herbivores.

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Human brain is considered unique. This extends to its growth pattern which has been claimed to be different from other mammals especially in its fast growth in early infancy.

Marsupials allow to study growth of the pouch young and thus to easily observe stages of growth corresponding to later fetal stages in eutherians. We studied the ontogeny of brain weight relative to body weight growth using pouch young sample of 43 koalas (*Phascolarctos cinereus*), 28 possums (*Trichosurus vulpecula*), and 36 tammar wallabies (*Macropus eugenii*) supplemented by 20-40 juveniles and adults for each species. When compared to other similar studies on marsupials and eutherians, two distinct patterns of mammalian brain growth were discerned.

When the brain weight and body weight values are expressed as a percentage of the respective adult values for brain and body size, the best fit for each studied marsupial and also for pigs, guinea pigs and rabbits is obtained with the same logarithmic curve of the following form:  $\text{Brain} = 15 \ln(\text{Body}) + 25$ , ( $R^2=0.93$ ) Brain growth of rhesus monkeys, rats, mice and humans each is best fitted by a continuous logistic curve with upper asymptote at 100%, inflection point at approximately 0 and velocity ranging from

0.1 to 0.2 ( $R^2=0.88-0.99$ ). The same logistic curve fits dogs and cats data somewhat better than the logarithmic one.

Therefore, humans like other primates share the brain growth pattern with omnivorous/carnivorous eutherians, in contrast to herbivorous mammals. Human brain growth seems unique only when considering absolute brain size in relation to age.

The fact that a common logistic curve characteristic for non-herbivorous mammals describes well the growth of human brain in relation to growth of body weight indicates that our brain growth pattern may be a simple result of our dietary adaptations, rather than be related to our intellectual uniqueness.

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Recently recovered hominid fossils from the site of Swartkrans. D.J. DE RUITER, Palaeo-Anthropology Research Group, Anatomical Sciences, University of the Witwatersrand, Johannesburg 2193, South Africa and C.K. BRAIN, Transvaal Museum, P.O. Box 413, Pretoria 0001, South Africa

Thirty-two new hominid specimens from the site of Swartkrans are described. A recent reexamination of the Swartkrans faunal collection housed in the Transvaal Museum in South Africa brought to light a series of hominid fossils that had either not been recognized as hominid or had been accidentally misplaced in the course of various excavations since the late 1930's. A further 3 hominid specimens of uncertain provenience, but possibly derived from Swartkrans, are also described.

The cranio-dental material includes a fragmented left hemi-mandible complete with very worn premolars and molars, as well as the roots of the canine and lateral incisor. An edentulous anterior mandibular corpus was found that may be associated with a previously recovered, but highly fragmented, hominid skull. Six complete hominid teeth were located, two of which are mandibular third molars showing no occlusal wear and incomplete root formation. These molars are almost certainly derived from the same individual. Several other fragmented teeth may also belong to this individual. Fourteen isolated tooth fragments were retrieved, some of which were refit to previously described hominid tooth fragments. The 3 hominids of uncertain provenience include 2 molar fragments and one complete, unworn canine with root unformed. The teeth are all consistent with *Paranthropus robustus*.

Ten post-cranial fossils were also recovered, comprised mostly of upper limb elements. These include 5 distal humeri, 2 of which possess complete, undistorted and only slightly damaged articular surfaces. Two proximal radii were found, one of which may be associated with one of the complete distal humeri. Two manual proximal phalanges were retrieved, as was a single femoral head with a portion of the neck preserved. At least two distinct size morphs are recognized in the post-cranial fossils that probably represent a taxonomic distinction and not sexual dimorphism.

Defining Gombe Stream National Park, Tanzania as a complex hybrid zone for two guenon species: *Cercopithecus ascanius schmidtii* and *Cercopithecus mitis doggetti*. K.M. DETWILER, Department of Anthropology, New York University and NYCEP, NY 10003

Hybridization between two sympatric forest primate species, redtails, *Cercopithecus ascanius schmidtii*, and blues, *C. mitis stuhlmanni*, has been recorded from three different research sites in Uganda: Budongo, Itwara, and Kibale Forests. At each site, hybrid individuals are rare. Hybridization at the Ngogo study site in the Kibale Forest is thought to reflect a shortage of female blue monkeys and consequent cross breeding by males.

Crosses between redtails and blues also occur at Gombe Stream National Park, Tanzania. For years primatologists working at Gombe have sighted hybrid individuals living among redtail social groups, but little is known about Gombe's *Cercopithecus* hybridization phenomenon. In 1996, I spent 664 hours in the Gombe forests looking for unhabituated groups of redtail and blue monkeys. I explored the 13 major stream valleys of Gombe National Park to determine the distribution of redtails, blues, and hybrids. I found hybrids living in both redtail and blue monkey social groups throughout both species' ranges within the park. I observed interspecific mating and suggest introgression occurs in both directions between redtails and blues. On several occasions, I observed hybrid females suckling infants, indicating that female hybrids are fertile.

Based on the results of this study and the fact that Gombe Stream National Park is a terrestrial island habitat, I define Gombe Stream as a localized sympatric hybrid zone for two guenon species, *Cercopithecus mitis* and *C. ascanius*. Thus, Gombe is of special interest to evolutionary primatologists because of its possible implications for speciation in African guenons.

Field work was funded by the Thomas J. Watson Foundation.

An experimental test of articular surface response to mechanical loading. M.J. DEVLIN and D.E. LIEBERMAN, Department of Anthropology, The George Washington University, Washington, DC 20052, and O.M. PEARSON, Department of Anthropology, University of New Mexico, Albuquerque, NM 87131.

How reliable are reconstructions of body mass and joint function based on articular surface areas? While the dynamic relationship between mechanical loading and cross-sectional geometry in long bones is well-established, the effect of loading on articular surface area has not been experimentally tested. The degree to which joints can change in size and shape is important because epiphyseal size is frequently used to estimate body mass and positional behavior in fossil species, including hominins. This study tests the hypothesis

that mechanical loading influences joint size by comparing articular surface areas of exercised and sedentary sheep from three age categories: juvenile, subadult, and adult ( $n=44$ ). It is expected that increases in area will be more pronounced in distal joints, which most likely encounter higher stresses than proximal joints. Also, the response is predicted to be more pronounced in younger individuals than in adults.

Joint surface areas were measured by making latex molds of articular surfaces of ten joints from each individual. Ten joints were modeled from each sheep. The molds were flattened, scanned and measured using computerized image analysis, and the area of each joint was then calculated. Areas were standardized by body mass and analyzed using Statview. These data were compared to cross-sectional geometrical data from each animal.

Analyses of Variance (ANOVA) between exercised and control individuals indicate no increases in joint surface area in response to mechanical loading in any age group. In contrast, significant differences in moments of inertia were detected between exercise and control groups in all age categories. The finding that articular surface area is more conservative than diaphyseal cross-sectional geometry has several implications. First, it supports the theory, based on comparative studies, that epiphyseal area is constrained throughout ontogeny. Second, this study indicates that joint surface area is related to locomotory behavior at the species level and to body mass at the individual level, while diaphyseal area is a more appropriate proxy for individual activity level. Finally, if articular surfaces are unable to compensate for loading through increases in area, then other aspects of joint morphology, such as subchondral bone density or trabecular orientation, must be responding to strain, particularly in distal joints.

Brain 'shape' and locomotion in primates.

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Conventional measures of relative brain size or encephalization are notoriously difficult to interpret in terms of their behavioral and ecological significance. Especially the relatively low scores obtained for the great apes appear counter-intuitive. Here the findings are presented of a multivariate morphometric analyses of the internal proportions or 'shape' of the brain in primates.

A multivariate analysis of 19 relative brain structure proportions in 921 specimens of 363 species of primates, insectivores, bats, tree- and elephant-shrews, has shown that different functionally integrated systems vary independently in the three major orders, thus demonstrating different evolutionary radiations in brain organization. Each radiation is associated with separate adaptive lifestyle convergences, in which unrelated species occupying similar behavioural niches have independently evolved similar internal brain proportions.

The primate radiation reflects a spectrum of locomotion that is also apparent in Oxnard's biomathematical studies of primate limbs: ranging from hindlimb-dominated leaping and squirrel-like scurrying, through quadrupedal running and jumping, to forelimb-dominated suspensory climbing and arm-swinging. This spectrum coincides with a proportional expansion of the neocortex, striatum, cerebellum and diencephalon relative to the medulla. Hence, it can be said to comprise an expansion of highest

levels of the distributed motor hierarchy, relative to the amount of somato-sensory and motor information that is exchanged with the body, suggesting that it may represent an increasing capacity to strategically plan and control complex motor actions. Such an interpretation fits the observed spectrum of flexibility and versatility of locomotion.

Several evolutionary convergences in brain 'shape' and locomotor habits are also implied. The most notable involves the New World atelines and Old World hominoids, which are widely considered to have independently evolved the same kind of forelimb-dominated, "quadrumanous" climbing-feeding complex.

**The Influence of Language and Geography on Anthropometric Variation of Native Americans from California.** P.C. DILLINGHAM, Department of Anthropology, The University of Tennessee, Knoxville, TN 37996.

In an earlier paper (Dillingham 1999), anthropometric data from Californian Native Americans collected in the 1920's by Edward Gifford and colleagues (Gifford 1926) was analyzed using principal components analysis and spatial autocorrelation techniques. Here, additional analyses were performed to determine what role language and geography may have played in the pattern of variation displayed by the data.

Calculations of Fst and multiple correlation extensions of the Mantel test (Smouse et al. 1986) were applied to twelve variables of the head, face, and body from samples of 15 tribes ranging from 9 to 36 in size. Before analysis the sexes were pooled and the data centered on the sex means. The Fst calculations were performed using Rmet. The Mantel tests were run using language, geography, and anthropometric distance matrices. Four analyses were run. First, to test for correlations between anthropometrics and geography; second, to test for correlations between anthropometrics and language; thirdly, to test for correlations between anthropometrics and geography controlling for language; and, finally to test for correlations between anthropometrics and language controlling for geography.

The Rmet program yielded an unbiased Fst of .24, which is even higher than the world average. This indicates that the tribes are more variable than the world's populations. Furthermore, the Mantel tests showed that only geography alone and geography controlling for language were significantly correlated with anthropometrics ( $p < .01$ ).

The inflated Fst could have been caused by either selection or plastic responses, while geography can influence selection or gene flow. Therefore, the pattern of variation in the data may be due to selection and/or plastic responses in conjunction with gene flow.

The relationship of life history variables to dental development in catarrhines. W. DIRKS, Anthropology, New York University, New York, NY, 10003

Dental development is undocumented in many species of extant catarrhines, although there is considerable interest in its application to understanding life history in fossil taxa. Eruption of the first molar has been demonstrated to correlate with weaning and brain size in primates, but the precise relationship of dental development to life history variables is unknown. Phylogeny and diet, particularly the degree of folivory, are expected to play an influence on both. Hominoids have slower life histories than cercopithecids and folivores grow more rapidly than frugivores or omnivores. Some aspects of dental development should reflect this.

In this study, I compare histologically derived data on the chronology of dental development in *Hylobates syndactylus*, *Papio hamadryas*, and *Semnopithecus entellus* to the timing of age at menarche and first reproduction in each species. Histological thin sections of the mandibular dentitions of one specimen of *S. entellus* with unworn  $M_1$  and three siamangs, one erupting  $M^1$ , one erupting  $I^2$ , and one erupting  $M_3$ , were analyzed by counting growth increments in polarized light. The age at initiation and completion of each tooth was determined, as well as age at death in each specimen to determine age at alveolar eruption of teeth.

$M^1$  erupted at 2.38yrs in one siamang, somewhat later than in a baboon, as predicted by the slower life histories of hominoids. The folivorous species *S. entellus* and *H. syndactylus* show acceleration of molar development relative to *P. hamadryas* and *H. lar*, respectively, but do so differently. *S. entellus* has rapid growth of the crowns and roots, as well as accelerated initiation of  $M_1$ , while *H. syndactylus* accelerates initiation of  $M_2$ .  $M_3$  erupts just before 4.67yrs in the *S. entellus* specimen, and at 5.15yrs in *H. syndactylus*. Menarche and first reproduction occur before the eruption of  $M_3$  in both cercopithecids, although at an earlier age in the langur than in the baboon. In the siamang, menarche may occur at around the age of eruption of  $M_3$ , while reproduction is delayed for several years afterwards.

The relationship of life history variables to dental development is complicated, as both are influenced by diet, phylogeny, and factors unique to each species. However, both cercopithecoids do show acceleration of reproduction relative to dental development, while both folivores show acceleration of dental development relative to that of frugivorous or omnivorous species in the same family.

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Primate Evolution: In and Out of Africa.

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Molecular sequence data, and the techniques used to analyze them, are now being used to answer a wide range of questions of interest to biological anthropologists. Inferences drawn from phylogenetic analyses of sequence data are applicable not only to

species phylogeny, but also to population genetics, biogeography, epidemiology, demography, and even paleontology. The rigorous analytical techniques that are now standard in molecular phylogenetics are beginning to be applied to questions in other fields.

Here we present a synthesis of molecular, paleontological, geological, morphological, and biogeographical data that supports what has been considered to be a minority view concerning hominoid evolutionary history. Our analysis suggests a dispersal out of Africa about twenty million years ago of the lineage leading to the living hominoids, followed by a dispersal back into Africa about ten million years ago of the common ancestor of the extant African ape clade, which includes humans. This scenario supports the contention that the early African Miocene hominoids are not direct ancestors of the living African hominoids. It also supports an African origin of the Old World monkeys, with dispersals to Eurasia of the Asian colobine and macaque lineages.

This scenario has been both disputed and supported by other authors. The logic of the arguments for and against our hypothesis will be discussed, and competing hypotheses will be evaluated using the computer-assisted phylogenetic and statistical techniques now employed in evolutionary biology. A robust phylogeny of the catarrhines can be used as a framework to infer important evolutionary phenomena, such as the origins of infectious diseases like SIV/HIV, as well as genetic adaptations to them by various species.

Relative postcranial joint size in australopithecine associated partial skeletons Stw 431 and AL 288-1. SETH D. DOBSON, Department of Anthropology, Washington University, St. Louis, MO 63130

The paucity of australopithecine associated postcranial remains makes it difficult to investigate the degree and pattern of interspecific variation in body proportions within *Australopithecus*. However, with the discovery of Stw 431, a large male partial skeleton of *A. africanus* from Member 4 Sterkfontein, it may be possible to gain new insight into this important issue. In this study, I address three questions relevant to the expression of species-level differences between Stw 431 and the *A. afarensis* partial skeleton AL 288-1. First, do apes and humans differ significantly in the limited set of proportions common to Stw 431 and AL 288-1? Second, are the proportions of these fossils ape-like or human-like? Finally, do the differences between Stw 431 and AL 288-1 fall within the expected range of variation for a single hominoid species, either *Pan troglodytes* or *Homo sapiens*?

The resultant comparison of joint proportions reveals significant differences between chimpanzees and humans. Discriminant function analysis classifies both



Stw 431 and AL 288-1 with the human sample based on elbow to hip proportions. However, based on elbow to lumbrosacral proportions, AL 288-1 groups with the human sample, while Stw 431 groups with chimpanzees. Randomization tests reveal no significant differences between Stw 431 and AL 288-1 given either a chimpanzee or human model of variation based on elbow to hip proportions. There are, however, significant differences between the two fossils given either model based on elbow to lumbrosacral proportions.

These findings, combined with previous studies of the australopithecine vertebral column, suggest that *A. africanus* had a significantly smaller first sacral centrum than *A. afarensis*, relative to several features strongly correlated with body size. Investigations of this kind may have important implications for early hominid phylogeny, locomotor biomechanics, and positional behavior.

Agriculture and dental caries? The case of rice in prehistoric Southeast Asia.

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The agricultural transition has long been recognised to have been an important period in human history. Its timing and consequences, including the effects on human health, have been intensively researched. In recent decades, this has included the idea that there is a universally positive correlation between the adoption of agriculture based on a carbohydrate staple crop and dental caries prevalence. This is mainly based on evidence from America, where maize was the staple crop. On the basis of evidence from prehistoric skeletal samples from a series of prehistoric sites in Southeast Asia, this simple correlation does not appear to apply in areas of the world where the staple carbohydrate is rice. Although we have looked only at dental caries, we suggest that caution be applied in the drawing of inferences about subsistence changes from dental health. Patterns reflecting the adoption of one starchy staple are not necessarily applicable to all such crops.

A physico-chemical fieldkit for ecological studies. N.J. DOMINY, N. YAMASHITA, H.C. ESSACKJEE, D. OSORIO, B.W. DARVELL and P.W. LUCAS. University of Hong Kong & University of Sussex.

Interest in the physico-chemical properties of plant foods and their influence on the feeding behavior of primates is long-standing. Physical properties of plant parts - size, weight, color and mechanical characteristics - must always be measured in the field because these change on storage. In contrast, chemical properties are almost always taken back to a laboratory after field-drying. This has stunted development: field tests would allow planning of experiments in the field. We built a fieldkit offering an almost complete physico-chemical characterization of foods that yield quick results with an accuracy not far below that of a home-based laboratory.

A portable S2000 spectrometer (Ocean Optics, Dunedin, FL), powered by a notebook computer via a PC card and coupled with a 12-v light source, allows both spectrophotometry for chemical tests and spectroradiometry for food color measurements with two small stages to hold samples or cuvettes. The fundamental requirement for chemical tests is water quality. Rainwater is the best source, which needs to be filtered and passed through a cheap deionizer (Model 101, Barnstead Thermolyne, Dubuque, IA). Battery-powered portable balances reading to 0.01g are adequate. Chemical tests are performed in microassay in Eppendorff tubes except for radial diffusion gels (by a method modified from Hagerman, 1987). A mechanical tester has been developed from that described by Darvell et al. (1996). The mechanical stage houses either a 10 N or 100 N load cell with an array of test jigs for a range of tensile and compressive tests. The kit is currently functioning well at Makerere University Biological Field Station, Kibale Forest, Uganda; Beza-Mahafaly Reserve, Madagascar and Marengo, Costa Rica.

mtDNA Variation in Ethiopian populations: Evidence of regional diversification of East African groups. B.P. DONHAM<sup>1</sup>, T.G. SCHURR<sup>2</sup>, D.L. DONHAM<sup>3</sup>, C.PANTER-BRICK<sup>4</sup>, D.C. WALLACE<sup>1</sup>. <sup>1</sup>Center for Molecular Medicine, Emory University, Atlanta, GA. 30322; <sup>2</sup>Southwest Foundation for Biomedical Research, San Antonio, TX. 78245-0549, <sup>3</sup>Dept. Anthropology, Emory University, Atlanta, GA. 30322; <sup>4</sup>Dept. Anthropology, Durham University, UK. DH1 3HN.

To elucidate the pattern of genetic variation in East Africa, we characterized the mitochondrial DNA (mtDNA) variation of 157 Ethiopians by restriction fragment length polymorphism (RFLP) and control region (CR) sequence analyses. Ninety-six of these samples were collected in the Maale area of southwest Ethiopia, whereas 61 samples were

collected in northern Ethiopia. While previous mtDNA studies of sub-Saharan populations showed that around two-thirds of their mtDNAs belonged to haplogroups L1 and L2 and the other one-third to haplogroup L3, which lacks the diagnostic HpaI 3592 site, this was not the case for the east African Ethiopians. Among Ethiopian groups, haplogroups L1 and L2 comprised only one-fourth of their mtDNAs, with most of the rest belonging to haplogroup L3. Comparisons of the CR sequence and RFLP haplotype data also showed that several putative L3 mtDNAs were derivatives of haplogroup L1 that had lost the diagnostic HpaI 3592 site. A number of the remaining Ethiopian samples had the RFLP motif of Asian macro-haplogroup M, i.e., the Dde I 10394 and AluI 10397 sites, suggesting that East Africa was either the source area for macro-haplogroup M mtDNAs, which were subsequently spread into east Asia, or that Asian mtDNAs were introduced into Africa more recently through genetic back-flow. We also observed a marked difference in the frequency of haplogroups L1, L2, and M in Ethiopian populations, with northern groups having 24% L1/L2 and 26% M and southern groups having 29% L1/L2 and only 6% M. The rest of the Ethiopian mtDNAs belonged to European haplogroups, with haplogroups H, I, T, and U being present in 15% of the northern samples, and haplogroups H and I accounting for 3% of the southern samples. These results reflect the significant regional differences in the genetic composition of Ethiopian populations. Moreover, they imply that East Africa represents the source area from which modern humans expanded into the rest of the Old World.

**Variation in scapular axillary border morphology.** S.P. DOUGHERTY, Department of Anthropology, and V.D. O'LOUGHLIN, Medical Sciences Program, Indiana University, Bloomington, IN 47405.

Trinkhaus (1977) was among the first to recognize three variations of the scapular axillary border: 1) the dorsal sulcus, 2) the ventral sulcus, and 3) the bisulcate pattern. The dorsal sulcus was initially interpreted as a by-product of biomechanical stress. However, other researchers have argued that these border variations are genetically determined, and as a result have used the axillary border in developing phylogenetic and taxonomic schema. This study attempts to understand further the developmental biology of the scapular axillary border.

Adult samples from two geographically separate archaeological populations were examined for their scapular axillary border morphology. Both populations sampled, the Arikara (n=25 individuals) and the Chirikof (n=55 scapulae), were noted for their participation in rigorous activities. The scapulae were examined by a single observer (SPD), and each scapular border pattern was recorded. Frequencies of each border pattern were calculated. In addition, small samples of neonates, infants, and juveniles from both populations were examined for comparative purposes.

In both the Chirikof and Arikara populations, the predominant scapular axillary border was the ventral sulcus form. However, variations in scapular morphology were observed, including some variations not documented previously. The *sole* scapular axillary border pattern found among the juveniles was the ventral sulcus pattern, although infants/neonates did not exhibit well-defined axillary border sulcus patterns at all. These results point to a previously unsuspected level of variation in the adult populations, thereby lending weight to the biomechanical stress hypothesis.

**A new approach to the analysis of the olecranon process in living hominoids and *A. afarensis*.** M.S. DRAPEAU  
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Traditionally, olecranon height (OH) is measured as the distance from the proximal tip of the ulna to either the center or the proximal limit of the trochlear articular surface. This method of measuring OH only estimates the length of the lever arm of the triceps brachii muscle (TBM) when the forearm is flexed at 90°, and does not accurately estimate the lever arm length of the TBM when the forearm is in other postures. I propose a method that estimates: (a) the maximum length of the lever arm for TBM (LMA), and (b) the degree of forearm flexion at which the TBM is the most effective (OA). LMA is measured from the center of rotation of the ulna in flexion to the most distant point of TBM insertion site. The angle that this moment arm makes with the long axis of the bone (OA) indicates the angle at which the TBM has the greatest leverage. An angle close to 90° indicates that the TBM has the greatest leverage in complete extension, while an angle near 180° indicates that the TBM has the greatest leverage at ninety degrees of elbow flexion.

The OA of modern *Homo* ( $\bar{x}=110$ ) and *Pan* ( $\bar{x}=102$ ) are significantly different from each other and from that of *Gorilla* ( $\bar{x}=92$ ) and *Pongo* ( $\bar{x}=91$ ). This suggests that *Gorilla* and *Pongo* emphasize more extended functional forearm postures. *Homo* is better adapted for more flexed postures, and *Pan* is intermediate. The relative moment arm of the TBM (LMA/ulna length distal to the trochlea) is similar in *Homo*, *Pan*, and *Gorilla*, and all three are higher than in *Pongo*. In comparison, relative olecranon height (OH/ulna length distal to the trochlea) is greater in *Homo*, then *Gorilla*, smaller in *Pongo*, and intermediate in *Pan*.

This new method shows that although African hominoid species emphasize different functional forelimb postures, lengths of the TBM lever arm are all equivalent. *Pongo* differs from other large hominoids since they combine small values of both LMA and OA.

Relative LMA values for *A. afarensis* are similar to that of extant African hominoids, while OA values ( $\bar{x}=127$ ) exceed the range of even *Homo*, indicating emphasis on more flexed forearm postures than any other species studied.